Fig. 1

Fig. 2

```
ICTB :   1  ATGACTGTCTGGCAAACTCTGACTTTTGCCCATTACCAACCCCAACAGTGGGGCCACAGC  60  (SEQ ID NO:2)
              ||  || |||||||  ||| | |||||  ||||| ||  ||||| | |||||||   ||
SLR  :  13  ATCTCTATCTGGCGATCGCTGATGTTTGGCGGTTTTGGCGGTTTTCCCCCAGGAATGGGGCCCGGGGC  72  (SEQ ID NO:4)

ICTB :  61  AGTTTCTTGCATCGGCTGTTTGGCAGCCTGC-GAGCTTGGCGGGCCTCCAGCCAGCTGTT  119
             |||| | |||| || ||| ||  || |||  ||  ||||  ||| |   ||
SLR  :  73  AGTGTGCTCCATCGTTTGGTGGGCTGGGGACAGAG-TTGGATACAGGCTAGTGTGCTCTG  131

ICTB : 120  GGTTTGGTCTGAGGCACTGGGT--GGCTTCTTGCTTGCTGCTGTCGTTCGGCTCCG  177
             - ||||||| |||  ||| ||| ||| || || | | ||||||
SLR  : 132  GCCCCACTTCGAGGCATTGGGTACGGCT-CTAG-TGGCAATAATTTTTATTGGCGGCTCCCC  189

ICTB : 178  TTTGTGCCCAGTTCCGCCCTAGGGTTGGGGCTAGCCGGATCGCG-GCCTATTGGGCCCT  236
             || ||  ||  |  || |||||||||||||||||||| || | ||| |||||| ||
SLR  : 190  TTCACCTCCACCACCATGTTGGGCATTTTTAT-GCTGCTCGTGTGGAGCCTTTTGGGCTCT  248

ICTB : 237  GCTCTCGCTGACAGATATCGATCTGCGCAAGCA---ACCCCCATTCACTGGCTGGTGCT  293
             |||  ||  || | ||| | ||  || | |||||||||| ||  ||  |   |  | ||
SLR  : 249  GCTGACCTTTGCTGAT--CAACCAG-GGAAGGGGTTTGACTCCATCGTTTTAGTTTT  305

ICTB : 294  GCTCTACTGGGGCGGTCGATGCCCTAGCAACGGGACTCTCACCCGTACGCGCTGCAGCTTT  353
             ||||||| || |  | | || |  |  | | || |||| |   |||||| || ||
SLR  : 306  TGCCTACTGGTGCATTTCGGCGATCGCCGTGGGATTTTCTCCGGTAAAAATGGCGGCGGC  365

ICTB : 354  AGTTGGGCTAGCCAAACTGAC-GCTC-TACCTGTTGGTTTTGCCCTAGCGGCTCGGGTT  411
             ||| |||| |||  ||| || |  ||| ||  |  ||||  | |||| ||
SLR  : 366  GTCGGGGTTAGCGAAATTAACAGCTAATTTATGTCTGTTTCTAC--TGGCGGCGAGGTTA  423

ICTB : 412  CTCCCGCAATCCCCGTCTGC-GATCGCTGCTGTTCTCGGTCGTCGTGATCACATCGCTTTT  470
             || ||  |  ||  ||||| || ||  | || |  || |||| |||| ||| |
SLR  : 424  TTGCAAAACAAACAATGCTTGAAC-CGGTTAGTAACCGTTGTTTTACTGGTAGGGCTATT  482
```

Fig. 2
(Continued)

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ICTB : 471   TGTCAGTGTCTACGGCCTCAACCAATGGATCTACGGCGTTGAAGAGCTGGCGACTTGGGT 530
                ||   | ||||| ||    | | || ||  ||  ||| ||  || ||||||
SLR  : 483   GGTGGGGAGTTACGGTCTGCGACAAACAGGTGGACGGGGTAGAACAGTTAGCCACTTGGAA 542

ICTB : 531   GGATCGCAACTCGGTGCCGACTTCACCTCACGGGTTTACAGCTATCTGGGCAACCCCAA 590
                || |||| |||   |    | |   ||  ||||| | || ||| | || |||||
SLR  : 543   TGACCCCACCTCTACCTTGGCCCAGGCCACTAGGGTATATAGCTTTTTAGGTAATCCCAA 602

ICTB : 591   CCTGCTGGCTGCTTATCTGGTGCCGACGACTGCCTTT-CTGCAGCAGCGATCGGGGGTGT 649
                || | || ||||| ||||||| | || |  |||  ||   |  |  |  | |
SLR  : 603   TCTCTTGGCGGCTTACCTGGTGCCCAAACTGCTCGG-GAGCAACCATGGTGATTGTTAACCTACTCTGT 661

ICTB : 650   GGCGCGGCTGGCTCCCCAAGCTGCTGGCGATCG-CTGCGACAGGTGCGAGCAGCTTATGT 708
                |||| | |||   |||||||| |||||| ||  | |  | | |  ||   | |||
SLR  : 662   GGCGACGGGTGGTGGCCAAACTGCTCGG-GAGCAACCATGGTGATTGTTAACCTACTCTGT 720

ICTB : 709   CTGATCCTCACCTACAGTCGCGCGGTGGCTGGGGTTTTGTCGCCATGATTTTTGTCTGG 768
                || | | ||| | || | | ||| | |  |||||   |  |   ||  ||   ||
SLR  : 721   CTCTTTTTTTACCCAGAGCCGGGGGCGGGGGGGTTGGCTAGCAGTGCCCTGGCCCTGGGGAGCTACCTTC 780

ICTB : 769   GCGGTTATTAGGGCTCTACTGGTTTCAACCCCGTCTACCCGCACCCTGGCGACGCTGGCTA 828
                | | |||||| | |   ||||||  |||||  |||||   |||  || | ||
SLR  : 781   CTGGCCCTTTGTTACTTCTGGTGTTACCCCAATTACCCAAATTTGGCAACGGTGGTCT 840

ICTB : 829   TTCCCAGTCGTATTGGGGTGGACTAGTCGCGCGGCTCTT-GGTGGCGGTGCTTGGACT--- 884
                | |   | | | |  ||  ||  | | |     |  |  | || | || |
SLR  : 841   TTGCCCCTGGC---GATCGCC--GTGGCGGTTATATTAGGTGGGGGGAGCGTTGATTGCG 894

ICTB : 885   -TG-AGCCGTTGCGCGTGTTGAGCATCTTTGTGGGGCGTGAAGACACGAGCAAC 942
                || | | | |  |   ||||||  || |||| |  | || ||
SLR  : 895   GTGGAACCGATTCGACTCAGGCCATGAGCATTTTTGCTGGGCGGGAAGACAGCAGTAAT 954
```

Fig. 2
(Continued)

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ICTB :  943  AACTTCCGGATCAATGTCTGGCTGGCGGTGCTGCAGATGATTCAAGATCGGCCTTGGCTG 1002
             !! !!!!!  !!!!!!!!! !!!   !  ! !!!    !  !! !!!!   !  !!!  !  -
SLR  :  955  AATTTCCGCATCAATGTTTGGGAAGGGGTAAAAGCCATGATCCGAGCCCGCCCTATCATT 1014

ICTB : 1003  GGCATCGGCCCCGGCAATACCGCCTTTAACCTGGTTTATCCCCTCTATCAACAGGCGCGC 1062
             !!!!! !!!!! !! !!  !!!!!!!!!!! !!!!  !!!    !  ! !!! !!!!  !!!
SLR  : 1015  GGCATTGGCCCAGGTAACGAAGCCTTTAACCAAATTTATCCTTACTATATGCGGCCCCGC 1074

ICTB : 1063  TTTACGGCGTTGAGCGCCTACTCCGTCCCGCTGGAAGTCGCGGTTGAGGGCGGACTACTG 1122
             !! !! !!  !!!! !!!! !!!!! !  !  !! !!! !   !! !!  !  !!   !!
SLR  : 1075  TTCACCGCCCCTGAGTGCCTATTCCATTTACCTAGAAATTTGGTGGAAACGGGTGTAGTT 1134

ICTB : 1123  GGCTTGA-CGGCCTTCGCTTGGCTGCT-GCTGGTCACGCGCGGTGACGGCGGTGCGGCAGG 1180
             !! ! !!  !! !!!! !  !!!!!!! ! !  !  !! !  !!  !!! ! !!  ! !! !!
SLR  : 1135  GGTTTTACCTGTATGCTC-TGGCTGTTGGCCGTTACCCTAGGCAAAGGC-GTAGAACTGG 1192

ICTB : 1181  TGAGCCGACTGCGCGGCGATCGCAATCCCC--AAGCCTTTGGTTGATGGCTAGCTTGGC 1238
             ! !  !! !!    !! !!!! !!!!      !!!! !  ! ! !!! !!   !! !!
SLR  : 1193  TTAAACG-CTGTCGC-CAAACCCTCGCCCCGGAAGGCATCTGGATTATGGGGGGCTTTAGC 1250

ICTB : 1239  CGGTTTGGCAGGAATGCTGGGTCACGGTCTGTTGATACCGTGCTCTATCGACCGGAAGC 1298
             !! !!! !!  !! !!  !!!! !!!!! !!   !! !!!! !  !!  !!  !!!!!!  -
SLR  : 1251  GGCGATCATCGGTTTGTTGGTCCACGGCATGGTAGTACAGTCTGGTACCGTCCCCCGGT 1310

ICTB : 1299  CAGTACGCTCTGGTGGCTCTGTATTGG--AGCGATCGCGAGTTTCTGG--CAGC-CCCAA 1353
             !! !!  ! !!!!!!!  ! !!! !!!    !! !! !!  !!! !!  !!!  !!!!
SLR  : 1311  GAGCACTTTGTGGTGG-TTGCTAGTGGCCATTG-TTGCTAGTCAGTCAGTGGGCCAGCGCCCAG 1368

ICTB : 1354  CCTTCCAAGCAACTCCCTCCAGAAGCCGAGCATTCAGACGAA 1395
             !! ! !!  !!!! !!  ! ! !!   !!!  !!!  !! !!
SLR  : 1369  GCCCGTTTGGAGGCCAGTAAAGAA---GAAAATGAGGACAAA 1407
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              +++W++L F + PQ+WG  S LHRL G  ++W...+S L    BALG  L+A+++ +APF
SLR  :   5    ISIWRSLMFGGFSPQENGRGSVLHRLVGWCQSWIQASVLWPHFEALGTALVAIIFIAPF   64

ICTB :  61    VPSSALGLGLAAIAAYWALLSLTDIDLRQATPIHRLVLLLYWGVDALATGLSPVRAALVG  120
              ++ LG+ +  A+WALL+ D  + TPIH LV YW + A+A G GPV+ AA  G
SLR  :  65    TSTTMLGIPMLLCGAFWALLTPADQPGKGLTPIHVLVFAYWCISAIAVGFSPVKMAAASG  124

ICTB : 121    LAKLTLYLLVPALAARVLRNPRLRSLLFSVVVITSLFVSVYGLNQMIYGVEELATWVDRN  180
              LAKLT  L +F LAAR+L+N +  + L +VV++  L V  YGL Q + GVE+LATW D
SLR  : 125    LAKLTANLCLFLLAARLLQNKQWLNRLVTVVLLVGLLVGSYGLRQQVDGVEQLATWNDPT  184

ICTB : 181    SVADFTSRVYSYLGNPNLLAAYLVPTTAFSAAAIGVWRGWLPKLLAIAATGASSLCLILT  240
              S   +RVYS+LGNPNLLAAYLVP T S +A+ VWR W PKLL      + LCL  T
SLR  : 185    STLAQATRVYSFLGNPNLLAAYLVPMTGLSLSALVVWRRWWPKLLGATMVIVNLLCLFFT  244

ICTB : 241    YSRGGWLGFVAMIFVWALLGLYWFQPRLPAPWRRWLFPVVLGGLVAVLLVAVLGLEPLRV  300
              SRGGWL  +A+ +  L  +W+ P+LP W+RW  P + V + A++ +EP+R+
SLR  : 245    QSRGGWLAVLALGATFLALCYFWMLPQLPKFWQRMSLPLAIAVAVILGGGALIAVEPIRL  304

ICTB : 301    RVLSIFVGREDSSNNFRINVWLAVIQMIQDRPWLGIGPGNTAFNLVYPLYQQARFTALSA  360
              R +SIF GREDSSNNFRINVW  V  MI+ RF +GIGPGN AFN +YP Y + RFTALSA
SLR  : 305    RAMSIFAGREDSSNNFRINVWEGVKAMIRARFIIGIGPGNEAFNQIYPYYMRPRFTALSA  364

ICTB : 361    YSVPLEVAVEGGLLGLTAPAWLLLVTAVTAVRQVSRLRRDRNFQAFWLMASLAGLAGMLG  420
              YS+ LE+ VE G++G T  WLL VT  V V R+ P+ W+M +LA + G+L
SLR  : 365    YSIYLEILVBTGVVGFTCMLWLLAVTLGKGVELVKRCRQTLAPEGIWIMGALARAIIGLLV  424

ICTB : 421    HGLFDTVLYRPEASTLWMLCIGAIASFWQPQPSKQLPPEAEHSDEKN  467
              HG+ DTV YRP STLWWL + +AS W ++  + B+ D+ +
SLR  : 425    HGMVDTVWYRPPVSTLWMLLVAIVASQWASAQARLBASKEENEDKPL  471
```
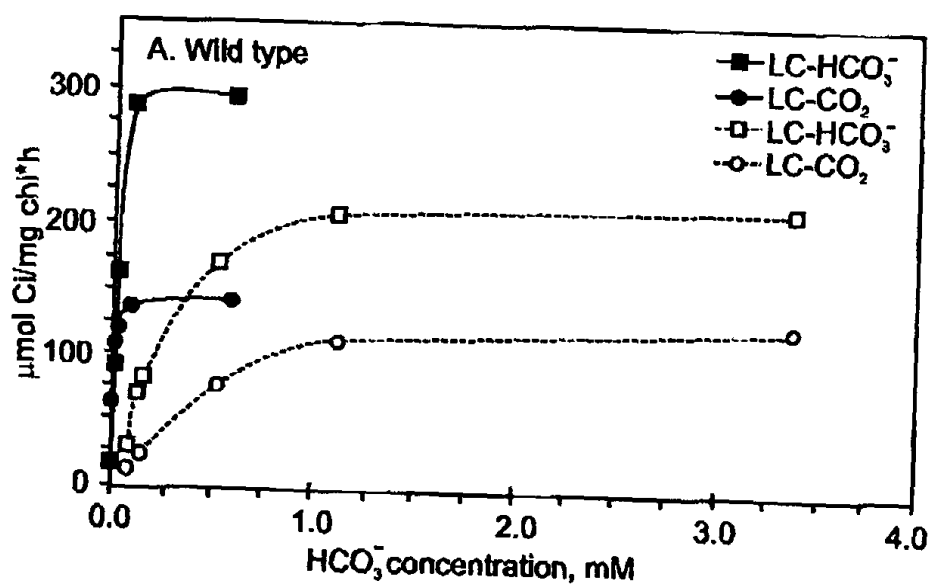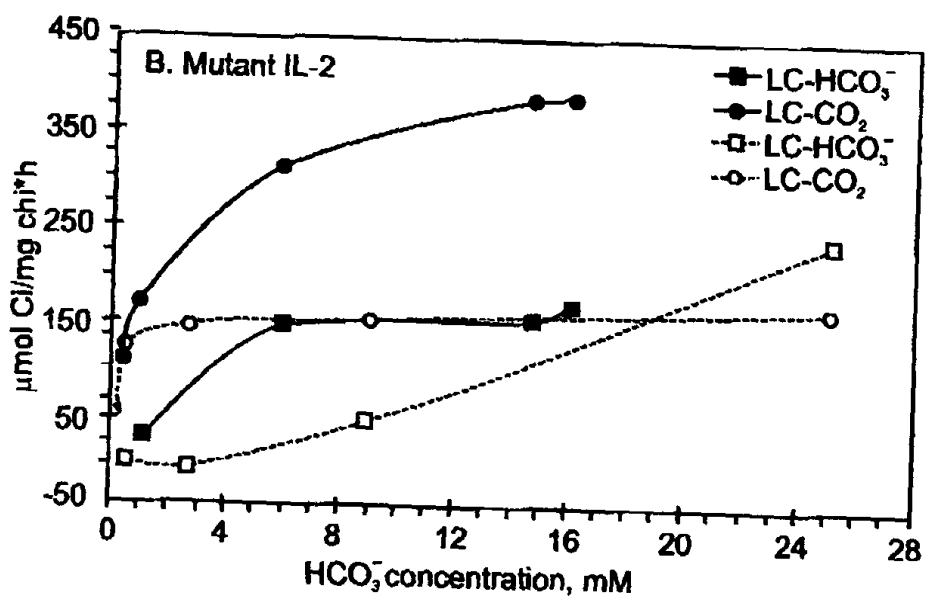
Fig. 3

Fig. 4a

Fig. 4b

Wild type   GGGCT-AGCCGCGATCGCGGCGGCCTATTGGGCCC   (SEQ ID NO:6)
IL-2 ApaI side   GGGCT-AG--G-GATCGC-GCCTATTGGGCCC   (SEQ ID NO:7)
IL-2 BamHI side   GGGCTCA----GATCGC-GCCTATTGGGCCC   (SEQ ID NO:8)
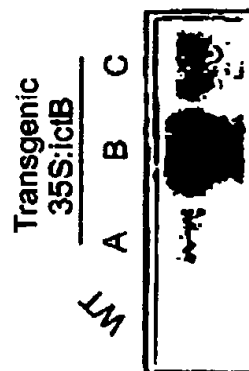IctB   G   L   A   A   I   A   A   Y   W   A   L   (SEQ ID NO:9)

Fig. 5

Transgenic
35S:ictB
WT   A   B   C

Fig. 6